Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1-56 (cancelled).

Claim 57 (previously presented): An isolated DNA sequence encoding a truncated insecticidal Cry2Ae protein consisting of the amino acid sequence of the protein of SEQ ID NO: 2 from amino acid position 1 to an amino acid position between amino acid position 625 and amino acid position 632.

Claim 58 (previously presented): An isolated DNA sequence encoding a truncated insecticidal Cry2Ae protein consisting of the amino acid sequence of the protein of SEQ ID NO: 2 from an amino acid position between amino acid position 1 and amino acid position 50 to amino acid position 632.

Claims 59-62 (cancelled).

Claim 63 (previously presented): A chimeric gene comprising the DNA sequence of claim 57, wherein said DNA sequence is under the control of a promoter which can direct expression of the gene in a plant cell.

Claim 64 (previously presented): The chimeric gene of claim 63, further comprising a DNA encoding a targeting or transit peptide which is operably-linked to said DNA encoding said Cry2Ae protein, wherein said targeting or transit peptide is a peptide targeting to the vacuole, mitochondrium, chloroplast, plastid, or for secretion.

Claim 65 (previously presented): A plant cell, plant or seed transformed to comprise the chimeric gene of claim 63.

Claim 66 (previously presented): A plant cell, plant or seed transformed to comprise the chimeric gene of claim 64.

Claim 67 (previously presented): The plant cell, plant or seed of claim 65, wherein said cell, plant or seed are of corn, cotton, rice, tobacco, oilseed rape, *Brassica* species, eggplant, soybean, potato, sunflower, tomato, sugarcane, tea, beans, strawberry, clover, cucumber, watermelon, pepper, oat, barley, wheat, dahlia, gladiolus, chrysanthemum, sugarbeet, sorghum, alfalfa, or peanut.

Claim 68 (previously presented): The plant cell, plant or seed of claim 66, wherein said cell, plant or seed are of corn, cotton, rice, tobacco, oilseed rape, *Brassica* species, eggplant, soybean, potato, sunflower, tomato, sugarcane, tea, beans, strawberry, clover, cucumber, watermelon, pepper, oat, barley, wheat, dahlia, gladiolus, chrysanthemum, sugarbeet, sorghum, alfalfa, or peanut.

Claim 69 (previously presented): A process for rendering a plant resistant to an insect, wherein said method comprises transforming plant cells with the chimeric gene of claim 63, and regenerating transformed plants from such cells.

Claim 70 (cancelled).

Claim 71 (currently amended): A chimeric gene comprising the following operably-linked elements:

(a) a [[35S]] promoter [[of]] region which is a DNA sequence from the Cauliflower Mosaic Virus 35S promoter;

(b) a DNA from the leader sequence ~~from~~ of the chlorophyll a/b binding protein gene from Petunia;

(c) a DNA ~~sequence~~ encoding the TpssuAT transit peptide;

(d) the DNA of claims 57 or 58~~, or a DNA encoding the protein of SEQ ID NO: 2 or an insecticidally effective fragment thereof,~~; and

(e) a 3' transcript termination and polyadenylation region which is a DNA sequence from the 3' transcript termination and polyadenylation region of the ~~35S gene from~~ Cauliflower Mosaic Virus 35S gene.

Claims 72 & 73 (cancelled).

Claim 74 (previously presented): The chimeric gene of claim 63, wherein said promoter is a promoter whose expression in plants is inducible by insect feeding.

Claim 75 (cancelled).

Claim 76 (previously presented): A process for rendering a plant resistant to an insect, comprising transforming plant cells with the chimeric gene of claim 71 or 74, and regenerating transformed plants from such cells which are resistant to insects.

Claim 77 (currently amended): A method for controlling insects comprising expressing in transformed plant cells an insecticidally-effective amount of said truncated insecticidal Cry2Ae protein encoded by the DNA of any one of claims 57 or 58, to control *Heliothis virescens*, *Helicoverpa zea*, *Helicoverpa armigera*, *Anticarsia gemmatalis* and *Ostrinia nubilalis*, *Chilo suppressalis*, *Chilo partellus*, *Scirpophaga incertulas*, *Sesamia inferens*, *Cnaphalocrocis medinalis*, *Marasmia patnalis*, *Marasmia exigua*, *Marasmia ruralis*, or *Scirpophaga innotata*.

Claim 78 (cancelled).

Claim 79 (previously presented): An isolated DNA sequence encoding a truncated insecticidal Cry2Ae protein consisting of the amino acid sequence of the protein of SEQ ID NO: 2 comprising a C-terminal deletion up to amino acid position 625.

Claim 80 (previously presented): An isolated DNA sequence encoding a truncated insecticidal Cry2Ae protein consisting of the amino acid sequence of the protein of SEQ ID NO: 2 comprising a N-terminal deletion up to amino acid position 50.

Claim 81 (previously presented): An isolated DNA sequence encoding a truncated insecticidal Cry2Ae protein consisting of the amino acid sequence of the protein of SEQ ID NO: 2 comprising an N-terminal deletion up to amino acid position 50 and a C-terminal deletion up to amino acid position 625.

Claim 82 (cancelled).

Claim 83 (currently amended): A method for protecting a plant of interest from ~~one or more~~ *Anticarsia gemmatalis* insects, comprising applying the polypeptide of SEQ ID NO: 2 or a transformed cell comprising a polynucleotide sequence encoding the polypeptide of SEQ ID NO: 2~~, wherein said one or more insects are *Helicopverpa armigera*, *Anticarsia gemmatalis*, *Sesamia nonagrioides* or combinations thereof~~.

Claim 84 (canceled).

Claim 85 (new): A chimeric gene comprising the following operably-linked elements:

(a) a promoter region which is a DNA sequence from the Cauliflower Mosaic Virus 35S promoter;

(b) a DNA encoding the TpssuAt transit peptide;

(c) a DNA encoding the amino acid sequence of the protein of SEQ ID NO: 2 from an amino acid position between amino acid position 1 and amino acid position 50 to amino acid position 632; and

(d) a 3' transcript termination and polyadenylation region which is a DNA sequence of the 3' transcript termination and polyadenylation region of the Cauliflower Mosaic Virus 35S gene.

Claim 86 (new): The chimeric gene of claim 85, wherein the DNA encoding the amino acid sequence of the protein of SEQ ID NO: 2 from an amino acid position between amino acid position 1 and amino acid position 50 to amino acid position 632 is the coding region of SEQ ID NO: 7, and wherein said TpssuAt transit peptide is inserted at the 5' end of said coding region.